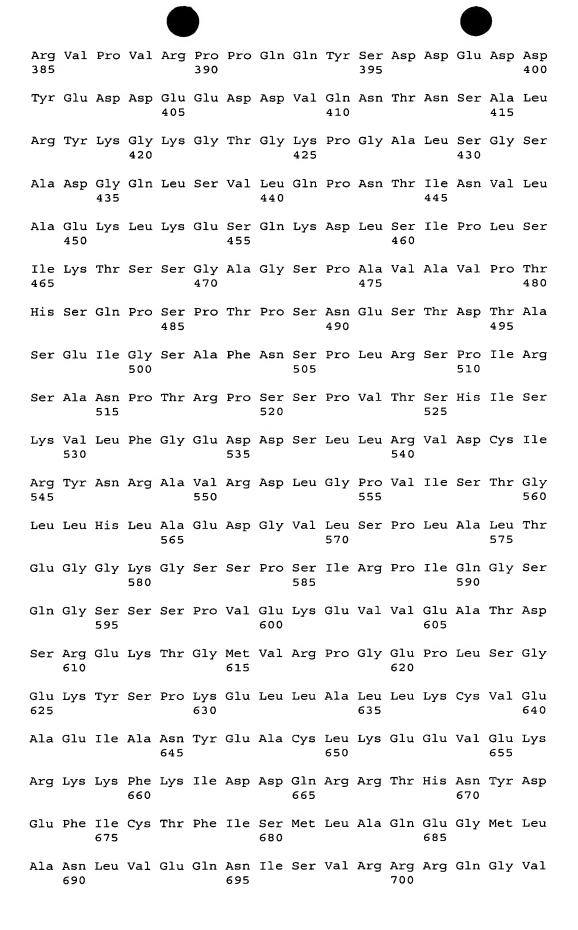
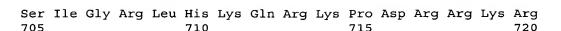
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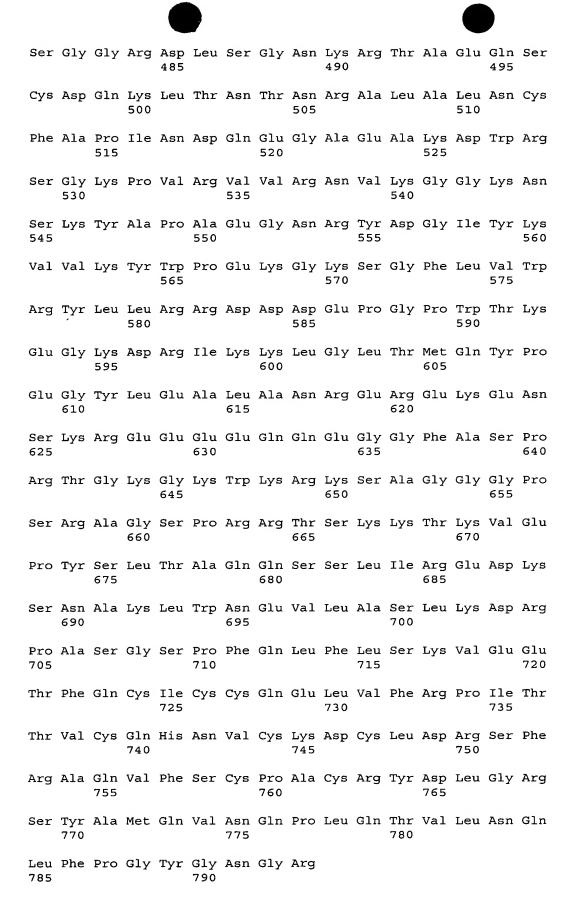
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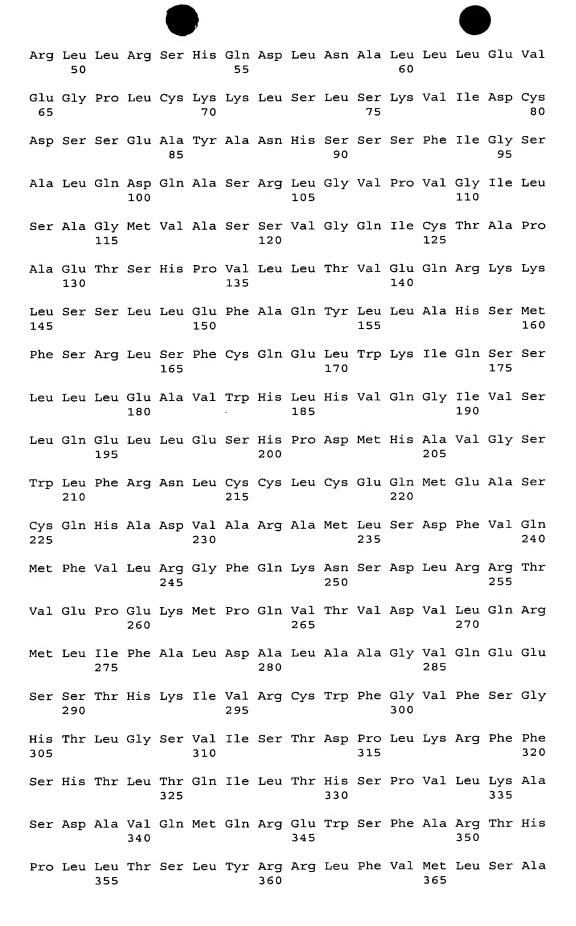


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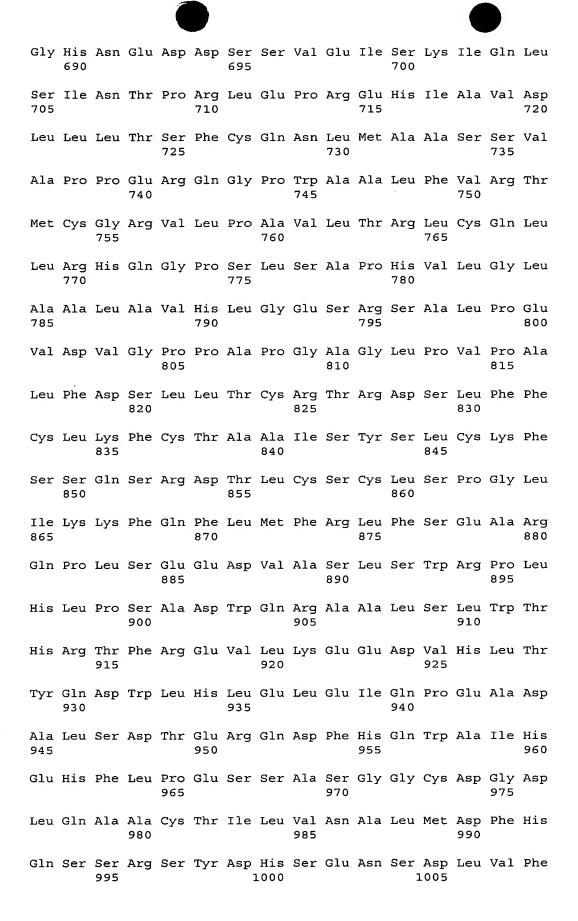
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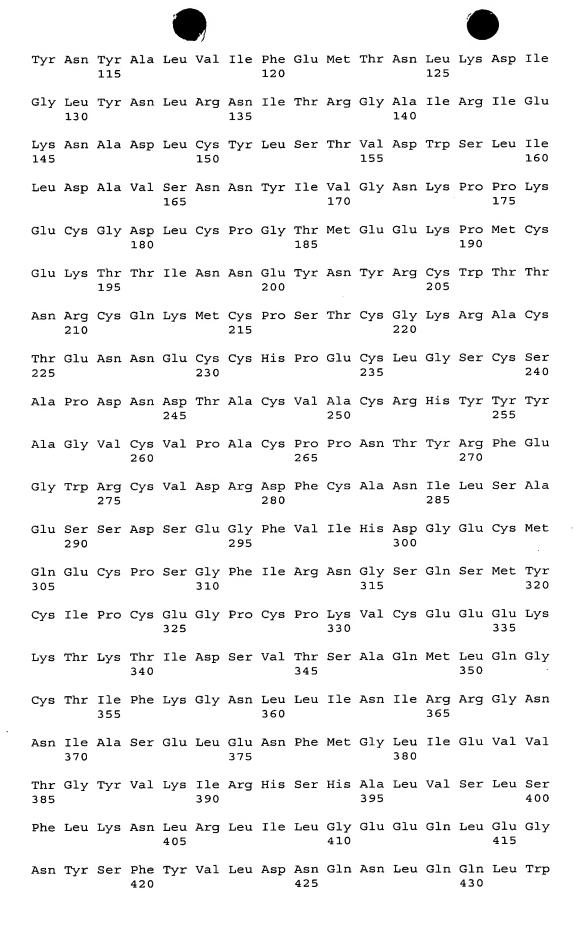


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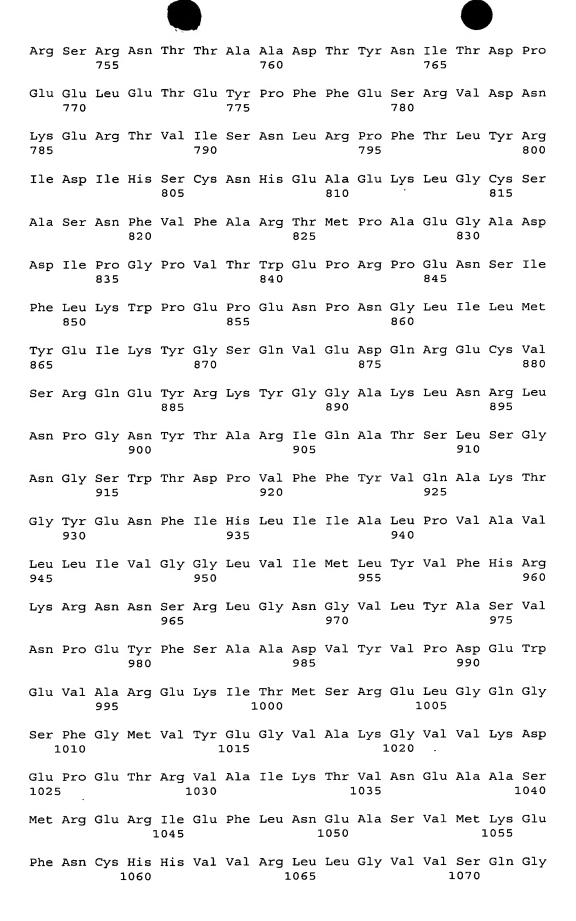


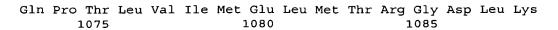
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Ser Lys Ala Glu Asp Tyr Arg Ser Tyr Arg Phe Pro Lys Leu Thr Val
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- Ser Asn Glu Gln Val Leu Arg Phe Val Met Glu Gly Gly Leu Leu Asp 1220 1225 1230
- Lys Pro Asp Asn Cys Pro Asp Met Leu Phe Glu Leu Met Arg Met Cys 1235 1240 1245
- Trp Gln Tyr Asn Pro Lys Met Arg Pro Ser Phe Leu Glu Ile Ile Ser 1250 1255 1260
- Ser Ile Lys Glu Glu Met Glu Pro Gly Phe Arg Glu Val Ser Phe Tyr 1265 1270 1275 1280
- Tyr Ser Glu Glu Asn Lys Leu Pro Glu Pro Glu Glu Leu Asp Leu Glu 1285 1290 1295
- Pro Glu Asn Met Glu Ser Val Pro Leu Asp Pro Ser Ala Ser Ser Ser 1300 1305 1310
- Ser Leu Pro Leu Pro Asp Arg His Ser Gly His Lys Ala Glu Asn Gly 1315 1320 1325
- Pro Gly Pro Gly Val Leu Val Leu Arg Ala Ser Phe Asp Glu Arg Gln 1330 : 1335 1340
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35 40 45

Trp Val Thr Leu Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His
50 55 60

His Arg Ile His His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr 65 70 75 80

Thr Gly Val Lys Val Pro Arg Asn Phe Arg Leu Leu Glu Glu Leu Glu 85 90 95

Glu Gly Gln Lys Gly Val Gly Asp Gly Thr Val Ser Trp Gly Leu Glu 100 105 110

Asp Asp Glu Asp Met Thr Leu Thr Arg Trp Thr Gly Met Ile Ile Gly 115 120 125

Pro Pro Arg Thr Ile Tyr Glu Asn Arg Ile Tyr Ser Leu Lys Ile Glu 130 135 140

Cys Gly Pro Lys Tyr Pro Glu Ala Pro Pro Phe Val Arg Phe Val Thr
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Lys Ile Asn Met Asn Gly Val Asn Ser Ser Asn Gly Val Val Asp Pro 165 170 175

Arg Ala Ile Ser Val Leu Ala Lys Trp Gln Asn Ser Tyr Ser Ile Lys 180 185 190

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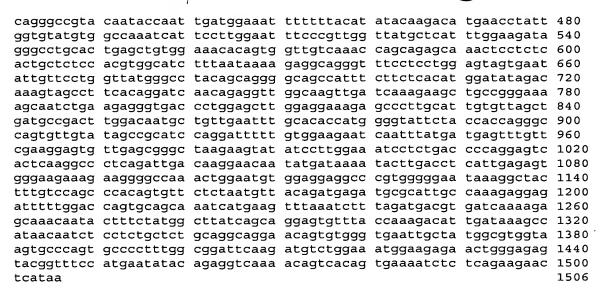
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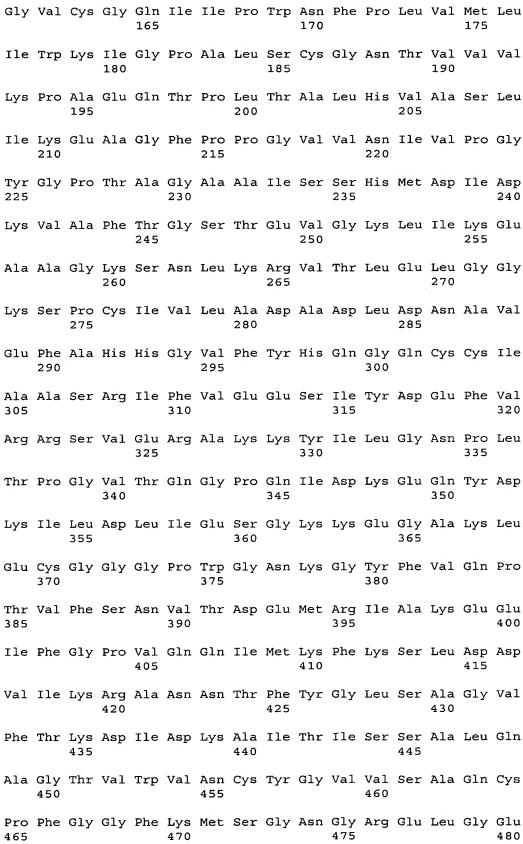
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             20
Val Ser Gly Lys Lys Phe Pro Val Phe Asn Pro Ala Thr Glu Glu Glu
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Leu Cys Gln Val Glu Glu Gly Asp Lys Glu Asp Val Asp Lys Ala Val
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Lys Ala Ala Arg Gln Ala Phe Gln Ile Gly Ser Pro Trp Arg Thr Met
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Asp Ala Ser Glu Arg Gly Arg Leu Leu Tyr Lys Leu Ala Asp Leu Ile
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Glu Arg Asp Arg Leu Leu Ala Thr Met Glu Ser Met Asn Gly Gly
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Lys Leu Tyr Ser Asn Ala Tyr Leu Ser Asp Leu Ala Gly Cys Ile Lys
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                                                125
Thr Leu Arg Tyr Cys Ala Gly Trp Ala Asp Lys Ile Gln Gly Arg Thr
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160







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Ser Gln Lys Asn Ser 500

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<213> Homo sapiens



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<223> similar to pyruvate kinase, muscle

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Leu Asp Ile Asp Ser Pro Pro Ile Thr Ala Arg Asn Thr Gly Ile Ile
35 40 45

Cys Thr Ile Gly Pro Ala Ser Arg Ser Val Glu Thr Leu Lys Glu Met 50 55 60

Ile Lys Ser Gly Met Asn Val Ala Arg Leu Asn Phe Ser His Gly Thr
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His Glu Tyr His Ala Glu Thr Ile Lys Asn Val Arg Thr Ala Thr Glu 85 90 95

Ser Phe Ala Ser Asp Pro Ile Leu Tyr Arg Pro Val Ala Val Ala Leu 100 105 110

Asp Thr Lys Gly Pro Glu Ile Arg Thr Gly Leu Ile Lys Gly Ser Gly
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Thr Ala Glu Val Glu Leu Lys Lys Gly Ala Thr Leu Lys Ile Thr Leu 130 135 140

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Tyr Lys Asn Ile Cys Lys Val Val Glu Val Gly Ser Lys Ile Tyr Val
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Leu Val Thr Glu Val Glu Asn Gly Gly Ser Leu Gly Ser Lys Lys Gly
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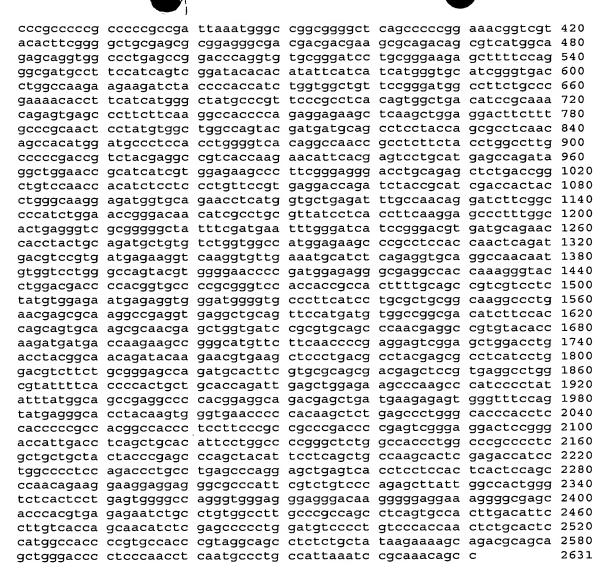
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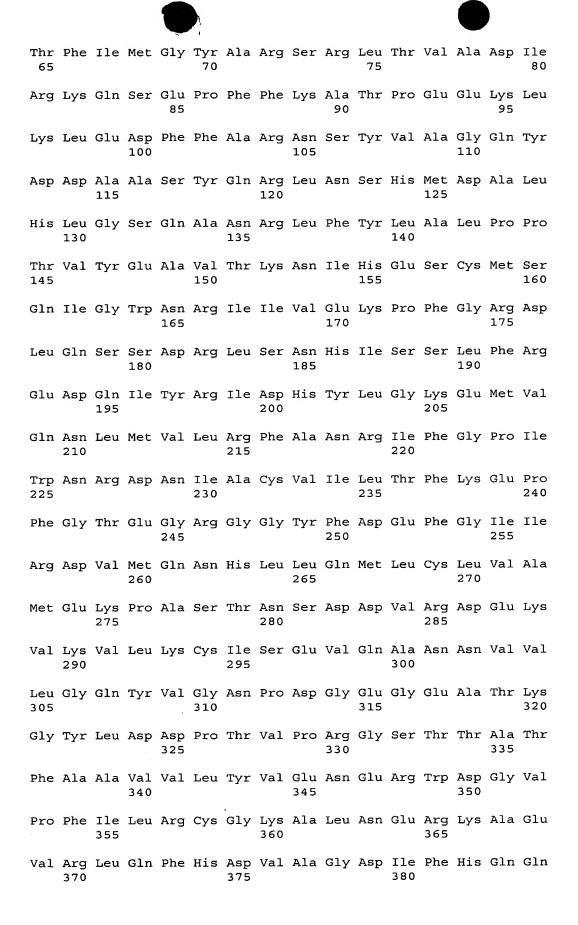
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Cys Glu Lys Gly Asp Ala Met Ile Met Glu Glu Thr Gly Lys Ile Phe 50 55 60

Lys Lys Glu Lys Glu Met Lys Lys Gly Ile Ala Phe Pro Thr Ser Ile 65 70 75 80

Ser Val Asn Asn Cys Val Cys His Phe Ser Pro Leu Lys Ser Asp Gln 85 90 95

Asp Tyr Ile Leu Lys Glu Gly Asp Leu Val Lys Ile Asp Leu Gly Val 100 105 110

His Val Asp Gly Phe Ile Ala Asn Val Ala His Thr Phe Val Val Asp 115 120 125

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Ala Ala His Leu Cys Ala Glu Ala Ala Leu Arg Leu Val Lys Pro Gly
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Asn Gln Asn Thr Gln Val Thr Glu Ala Trp Asn Lys Val Ala His Ser 165 170 175

Phe Asn Cys Thr Pro Ile Glu Gly Met Leu Ser His Gln Leu Lys Gln 180 185 190

His Val Ile Asp Gly Glu Lys Thr Ile Ile Gln Asn Pro Thr Asp Gln
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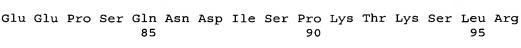


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Lys Pro Lys Lys Met Lys Lys Glu Lys Glu Met Asn Gly Glu Thr Arg 130 135 140

Glu Lys Ser Pro Lys Leu Lys Asn Gly Phe Pro His Pro Glu Pro Asp 145 150 155 160

Cys Asn Pro Ser Glu Ala Ala Ser Glu Glu Ser Asn Ser Glu Ile Glu 165 170 175

Gln Glu Ile Pro Val Glu Gln Lys Glu Gly Ala Phe Ser Asn Phe Pro 180 185 190

Ile Ser Glu Glu Thr Ile Lys Leu Leu Lys Gly Arg Gly Val Thr Phe
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Arg Gly Arg Ala Pro Gln Val Leu Val Leu Ala Pro Thr Arg Glu Leu 260 265 270

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Val Ala Cys Phe Tyr Gly Gly Thr Pro Tyr Gly Gly Gln Phe Glu Arg 290 295 300

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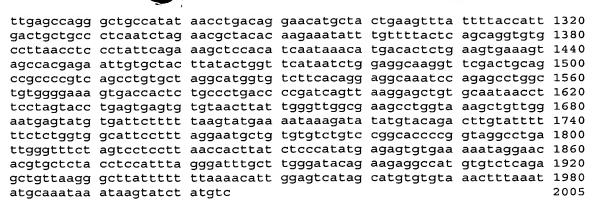
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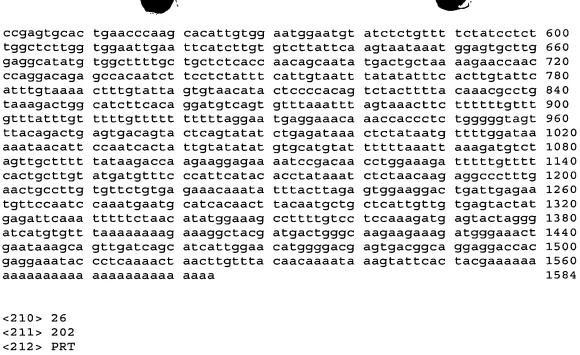


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Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg Phe Val Trp
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Phe Phe Ser Gly Ile Val Gly Gly Leu Leu Met Leu Leu Pro Ala
Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly Cys Cys Gly
65
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His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser Val Leu Ala
Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile Val Ala Ala
            100
                                105
                                                     110
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Ser Leu Phe Ser Ile Leu Leu Ala Leu Gly Gly Ile Glu Phe Ile Leu 165 170 175

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Val Asp Thr Ser Ala Gln Ala Ala Pro Gln Thr Tyr Ala Glu Tyr Ala
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	Lys	Ser	Asn	Ser 100	Ile	Ile	Val	Ser	Pro 105	Arg	Gln	Arg	Gly	Asn 110	Pro	Val
	Leu	Lys	Phe 115	Val	Arg	Asn	Val	Pro 120	Trp	Glu	Phe	Gly	Asp 125	Val	Ile	Pro
	Asp	Tyr 130	Val	Leu	Gly	Gln	Ser 135	Thr	Cys	Ala	Leu	Phe 140	Leu	Ser	Leu	Arg
	Tyr 145	His	Asn	Leu	His	Pro 150	Asp	Tyr	Ile	His	Gly 155	Arg	Leu	Gln	Ser	Leu 160
	Gly	Lys	Asn	Phe	Ala 165	Leu	Arg	Val	Leu	Leu 170	Val	Gln	Val	Asp	Val 175	Lys
	Asp	Pro	Gln	Gln 180	Ala	Leu	Lys	Glu	Leu 185	Ala	Lys	Met	Cys	Ile 190	Leu	Ala
	Asp	Cys	Thr 195	Leu	Ile	Leu	Ala	Trp 200	Ser	Pro	Glu	Glu	Ala 205	Gly	Arg	Tyr
	Leu	Glu 210	Thr	Tyr	Lys	Ala	Tyr 215	Glu	Gln	Lys	Pro	Ala 220	Asp	Leu	Leu	Met
	Glu 225	Lys	Leu	Glu	Gln	Asp 230	Phe	Val	Ser	Arg	Val 235	Thr	Glu	Cys	Leu	Thr 240
	Thr	Val	Lys	Ser	Val 245	Asn	Lys	Thr	Asp	Ser 250	Gln	Thr	Leu	Leu	Thr 255	Thr
	Phe	Gly	Ser	Leu 260	Glu	Gln	Leu	Ile	Ala 265	Ala	Ser	Arg	Glu	Asp 270	Leu	Ala
	Leu	Cys	Pro 275	Gly	Leu	Gly		Gln 280		Ala	Arg	Arg	Leu 285		Asp	Val
	Leu	His 290	Glu	Pro	Phe	Leu	Lys 295	Val	Pro							
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	<220 <223	3> ce			cer a			nctic CDNA	onal	hit	from	n ret	rovi	ral		
	. 4 0 0															

181

ccagtgtgct ggaaaggagg aagatateet ggetggeact ettteagttg acagagagtg 60 aceteagget ggggeggete etecteegtg tggeecegga teageacace aggetgetge 120 etttegettt ttacagtett eteteetact teeatgaaga egeggettte eageacagtg 180

<400> 29

g



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<210> 30
<211> 603
<212> DNA
<213> Homo sapiens
<220>
<223> cell tracker assay functional hit from retroviral
      screen DDX9 partial cDNA
<400> 30
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cccctaccac cwcctcqctq gaatccccca gatcctctgt agcctccact aggccctctg 120
taqteteete caqaqttqee tetaaaqeea eetegggaga eteetetata geeteeacca 180
acacctgcac catatectgc ecgaaaggag ttggegetge caccatagee teegetacea 240
tagcetecae tgetatagee acegeatage etceaecaet gtaactagaa ceteceette 300
tatatccgct tccattgtcg tatcgggcca tcttgggagg acgtggacca tctccatgcc 360
gtgtactgcc aatcataagg ttgataccag cagctgaggg tctagagatc tgacggatca 420
tgttcagcat acgttcattt acggggtcca actggctgat gatagcaggt tgtttggtta 480
cttcaacaac caaagcctcc atggctgccc ggagaccagt gatacaggca gcagcttcat 540
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tgg
<210> 31
<211> 145
<212> DNA
<213> Homo sapiens
<220>
<223> cell tracker assay functional hit from retroviral
      screen IGF1R partial cDNA
<400> 31
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gcatcgatat ccacagctgc aaccacgagg ctgagaagct gggctgcagc gcctccaact 120
tcqtctttqc tttccagcac agtqq
                                                                   145
<210> 32
<211> 269
<212> DNA
<213> Homo sapiens
<220>
<223> cell tracker assay functional hit from retroviral
      screen UBEV2V1 partial cDNA
<400> 32
ccaqtgtgct ggaaaggtgc ttctgggtat ttaggtccac attctatttt aaggctgtat 60
atteggtttt cataaattgt tettggagge ecaattatea teeetgteea tettgtaaga 120
tqtcatqtct tcqtcatctt ctagacccca gctaactqtg ccatctccta ctcctttctg 180
gccttcttcg agattcctcc aacagtcgga aattgcgagg gactttatac atcccgagcc 240
                                                                   269
cgtggtggct gccctttcca gcacactgg
<210> 33
<211> 499
<212> DNA
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<213> Homo sapiens





<220> <223> cell tracker assay functional hit from retroviral screen aldehyde dehydrogenase partial cDNA <400> 33 ccagtgtgct ggaaaggagc aaactcctct cactgctctc cacgtggcat ctttaataaa 60 agaggcaggg tttcctcctg gagtagtgaa tattgttcct ggttatgggc ctacagcagg 120 ggcagccatt tcttctcaca tggatataga caaagtagcc ttcacaggat caacagaggt 180 tggcaagttg atcaaagaag ctgccgggaa aagcaatctg aagagggtga ccctggagct 240 tggaggaaag agcccttgca ttgtgttagc tgatgccgac ttggacaatg ctgttgaatt 300 tgcacaccat ggggtattct accaccaggg ccagtgttgt atagccgcat ccaggatttt 360 tgtggaagaa tcaatttatg atgagttttg ttcgaaggag tgttgagcgg gctaagaacg 420 tatateettg gaaacateet etgaceecag gagteaetea aaggeeetea gattgacaag 480 gactttccag acacagtgg <210> 34 <211> 425 <212> DNA <213> Homo sapiens <220> <223> cell tracker assay functional hit from retroviral screen pyruvate dehydrogenase partial cDNA <400> 34 ccaqtqtqct qqaaaqqctq cccacttcca ccaccttgca gatgttcttg tagtccagcc 60 acaqqatqtt ctcqtcacac ttttccatqt aqqcgttatc caqcgtgatt ttgaqagtgg 120 ctcccttctt cagetccace tetgcagtge egetgeeett gatgageeea gtteggatet 180 caggtccttt agtgtctaga gccacagcaa cgggccggta gaggatgggg tcagaagcaa 240 agettteegt ggetgtgege acattettga tggteteege atggtaetea tgagtteeat 300 gagagaagtt cagacgagcc acattcattc cagacttaat catctccttc aacgtctcca 360 ctggatcggg aagctgggcc aatggtacag atgatgccag tgttccgggc tttccagcac 420 agtgg <210> 35 <211> 238 <212> DNA <213> Homo sapiens <220> <223> cell tracker assay functional hit from retroviral screen G6PD partial cDNA <220> <221> modified base <222> (1)..(238) <223> n = g, a, c or t<400> 35 ccaqtqtqct qqaaactttc caqttctcca tqqccaccan acacaqcatc tqcaqtaggt 60 ggttctgcat cacgtcccgg atgatcccaa attcatcgaa atagcccccg cgaccctcag 120 tgccaaaggg ctccttgaag gtgaggataa cgcaggcgat gttgtcccgg ttccanatgg 180 ggccgaagat cctgttggca aatctcagca ccatgaggtt ctctttccag cacagtgg <210> 36 <211> 491

<212> DNA





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<220>
<223> Description of Artificial Sequence:G3-2D8 sequence
      with C-terminus of GFP, partial BAP-1 sequence
<220>
<221> modified base
<222> (69)
<223> n = g, a, c or t
<400> 36
gagttcgtga ccgccgccgg gatcactctc ggcatggacg agctgtacaa ggaggaggcc 60
gccaaggeng gtggcagegg tggctccagt gtgctggaaa gctaagggca gagttggtgt 120
tctgcacgtc atcctctcgt catcctcata gtcatcctca tcatctgagt actgctgggg 180
tgggcggact ggaactcggc tgcggccac acctgccgcc aggtcttctt cctcctgcat 240
gggggacttg gcataattgt gattgtctag aaaggccggc agccgctgga caatgggagt 300
ggggttgggg tgaaccccat tgaggctgct gcctggaggc taccactagc ttgggtttgt 360
tgggagggct gtgggatggg gcttgtgcgc atgaaccagc cgcctcctcg caccatctgt 420
gtggttgccc tcagaggctg caggggccct gtttgcttcc agcaccagcg gggacctttc 480
cagcacagtg g
<210> 37
<211> 34
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:G3-2D8 sequence
      with C-terminus of GFP, partial BAP-1 sequence
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu
                                 25
Glu Ser
<210> 38
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:BstXI linker
<400> 38
                                                                   16
ccagtgtgct ggaaag
<210> 39
<211> 16
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:BstXI linker
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<400> 39
ctttccagca cagtgg 16

<210> 40

<211> 136

<212> PRT

<213> Homo sapiens

<220>

<223> G1-2635 sequence, partial NP95 sequence

<400> 40

Ala Glu Gln Ser Cys Asp Gln Lys Leu Thr Asn Thr Asn Arg Ala Leu 1 5 10 15

Ala Leu Asn Cys Phe Ala Pro Ile Asn Asp Gln Glu Gly Ala Glu Ala 20 25 30

Lys Asp Trp Arg Ser Gly Lys Pro Val Arg Val Val Arg Asn Val Lys
35 40 45

Gly Gly Lys Asn Ser Lys Tyr Ala Pro Ala Glu Gly Asn Arg Tyr Asp 50 60

Gly Ile Tyr Lys Val Val Lys Tyr Trp Pro Glu Lys Gly Lys Ser Gly 65 70 75 80

Phe Leu Val Trp Arg Tyr Leu Leu Arg Arg Asp Asp Glu Pro Gly
85 90 95

Pro Trp Thr Lys Glu Gly Lys Asp Arg Ile Lys Lys Leu Gly Leu Thr
100 105 110

Met Gln Tyr Pro Glu Gly Tyr Leu Glu Ala Leu Ala Asn Arg Glu Arg
115 120 125

Glu Lys Glu Asn Ser Lys Arg Glu 130 135

<210> 41

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<223> G2-2F3 sequence, partial FANCA sequence

<400> 41

Arg Lys Ile Ser Trp Leu Ala Leu Phe Gln Leu Thr Glu Ser Asp Leu 1 5 10 15

Arg Leu Gly Arg Leu Leu Arg Val Ala Pro Asp Gln His Thr Arg
20 25 30

Leu Leu Pro Phe Ala Phe Tyr Ser Leu Leu Ser Tyr Phe His Glu Asp
35 40 45

Ala



-22As

<223> Description of Artificial Sequence:G3-2H6 sequence
 with C-terminus of GFP, partial DDX9 sequence

<400> 42

<210> 42 <211> 552 <212> DNA

gagttcgtga ccgccgcgg gatcactctc ggcatggacg agctgtacaa ggaggaggcc 60 gccaaggccg gtggcagcgg tggctccagt gtgctggaaa gcgccacctc ctcttccctg 120 tccaaagtag ccagttccat aggccccct accactcct cgctggaatc ccccagatcc 180 tctgtagcct ccactaggcc ctctgtagtc tcctccagag ttgcctctaa agccacctcg 240 ggaggactcct ctatagcctc caccaacacc tgcaccatat cctgcccgaa aggagttggc 300 gctgccacca tagcctccgc taccatagcc tccactgcta tagccaccgc atagcctcca 360 ccactgtaac tagaacctcc ccttctatat ccgcttccat tgtcgtatcg ggccatcttg 420 ggaggacgtg gaccatctcc atgccgtgta ctgccaatca taaggttgat accagcagct 480 gagggtctac agatctgacg gatcatgttc agcatagtt cattacggg gtccaactgg 540 ctgatggatag ca

<210> 43

<211> 117

<212> PRT

<213> Artificial Sequence

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2H6 sequence
 with C-terminus of GFP, partial DDX9 sequence

<400> 43

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 1 5 10 15

Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu 20 25 30

Glu Ser Ala Thr Ser Ser Ser Leu Ser Lys Val Ala Ser Ser Ile Gly
35 40 45

Pro Pro Thr Thr Ser Ser Leu Glu Ser Pro Arg Ser Ser Val Ala Ser 50 55 60

Thr Arg Pro Ser Val Val Ser Ser Arg Val Ala Ser Lys Ala Thr Ser 65 70 75 80

Gly Asp Ser Ser Ile Ala Ser Thr Asn Thr Cys Thr Ile Ser Cys Pro 85 90 95

Lys Gly Val Gly Ala Ala Thr Ile Ala Ser Ala Thr Ile Ala Ser Thr
100 105 110

Ala Ile Ala Thr Ala 115

<210> 44

<211> 38

<212> PRT

<213> Homo sapiens



<220>

<223> G3-2H2 1 sequence, partial IGF1R sequence

<400> 44

Glu Arg Thr Val Ile Ser Asn Leu Arg Pro Phe Thr Leu Tyr Arg Ile 1 5 10 15

Asp Ile His Ser Cys Asn His Glu Ala Glu Lys Leu Gly Cys Ser Ala 20 25 30

Ser Asn Phe Val Phe Ala 35

<210> 45

<211> 347

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2G2/2H2
 sequence with C-terminus of GFP, partial UBE2V1
 sequence

<400> 45

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<210> 46

<211> 75

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:G3-2G2/2H2
 sequence with C-terminus of GFP, partial UBE2V1
 sequence

<400> 46

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr 1 5 10 15

Lys Glu Glu Ala Ala Lys Ala Gly Gly Ser Gly Gly Ser Ser Val Leu 20 25 30

Glu Arg Cys Phe Trp Val Phe Arg Ser Thr Phe Tyr Phe Lys Ala Val 35 40 45

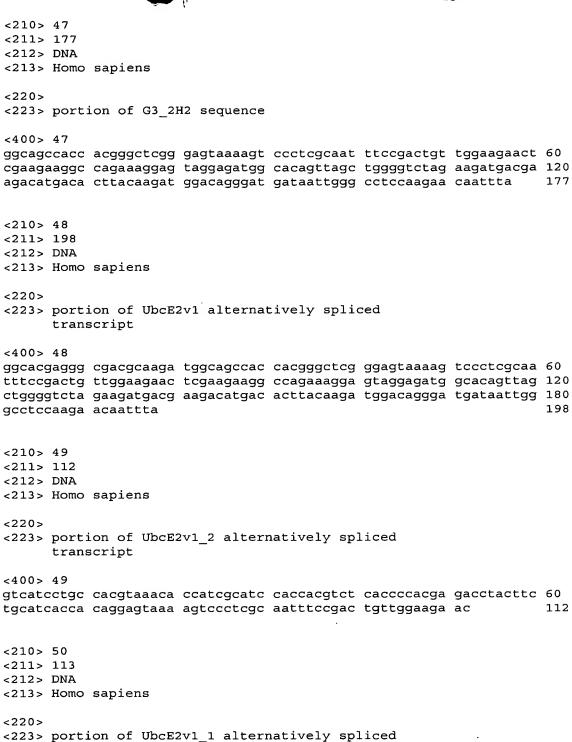
Tyr Ser Val Phe Ile Asn Cys Ser Trp Arg Pro Asn Tyr His Pro Cys 50 55 60

Pro Ser Cys Lys Cys His Val Phe Val Ile Phe 65 70 75



transcript

<400> 50



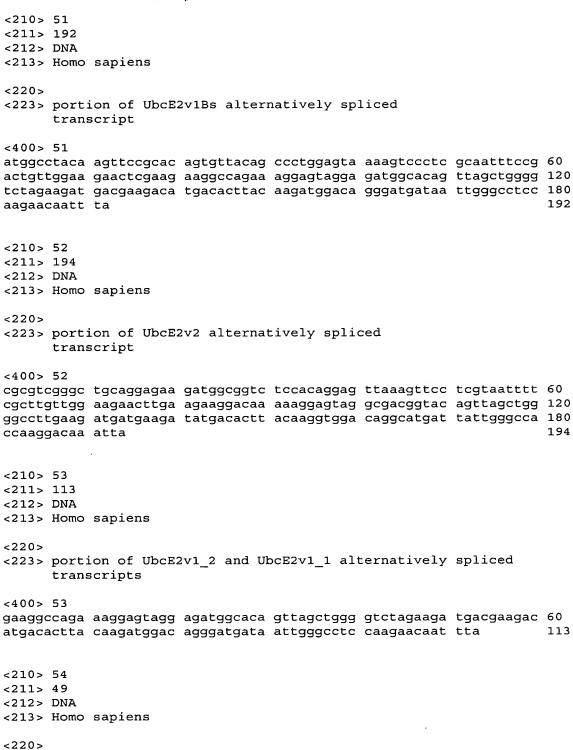
aagcgtctta cctgaagtca caaagcaaac tgagtgatga aggaagactt gaacctagaa 60

aatttcactg caaagggagt aaaagtccct cgcaatttcg actgttggaa gaa



<223> portion of G3_2H2 sequence

cgaatataca gccttaaaat agaatgtgga cctaaatacc cagaagcac



49



<210> 55

<211> 60

<212> DNA

<213> Homo sapiens

<220>

400 > 55

cgaatataca gccttaaaat agaatgtgga cctaaatacc cagaagcacc cccctttgta 60

<210> 56

<211> 60

<212> DNA

<213> Homo sapiens

<220>

<223> portion of UbcE2v2 alternatively spliced
 transcript

<400> 56

agaatatata gcctgaaagt agaatgtgga cctaaatacc cagaagctcc tccgtcagtt 60

<210> 57

<211> 225

<212> PRT

<213> Homo sapiens

<220>

<223> Uch-13 sequence

<400> 57

Met Glu Gly Gln Arg Trp Leu Pro Leu Glu Ala Asn Pro Glu Val Thr 1 5 10 15

Asn Gln Phe Leu Lys Gln Leu Gly Leu His Pro Asn Trp Gln Phe Val

Asp Val Tyr Gly Met Asp Pro Glu Leu Leu Ser Met Val Pro Arg Pro 35 40 45

Val Cys Ala Val Leu Leu Phe Pro Ile Thr Glu Lys Tyr Glu Val
50 55 60

Phe Arg Thr Glu Glu Glu Lys Ile Lys Ser Gln Gly Gln Asp Val 65 70 75 80

Thr Ser Ser Val Tyr Phe Met Lys Gln Thr Ile Ser Asn Ala Cys Gly 85 90 95

Thr Ile Gly Leu Ile His Ala Ile Ala Asn Asn Lys Asp Lys Met His
100 105 110

Phe Glu Ser Gly Ser Thr Leu Lys Lys Phe Leu Glu Glu Ser Val Ser 115 120 125

Met Ser Pro Glu Glu Arg Ala Arg Tyr Leu Glu Asn Tyr Asp Ala Ile 130 135 140





Arg Val Thr His Glu Thr Ser Ala His Glu Gly Gln Thr Glu Ala Pro 145 150 155 160

Ser Ile Asp Glu Lys Val Asp Leu His Phe Ile Ala Leu Val His Val 165 170 175

Asp Gly His Leu Tyr Glu Leu Asp Gly Arg Lys Pro Phe Pro Ile Asn 180 185 190

His Gly Glu Thr Ser Asp Glu Thr Leu Leu Glu Asp Ala Ile Glu Val 195 200 205

Cys Lys Lys Phe Met Glu Arg Asp Pro Asp Glu Leu Arg Phe Asn Ala 210 215 220

Ile 225

<210> 58

<211> 231

<212> PRT

<213> Homo sapiens

<220>

<223> portion of BAP-1

<400> 58

Met Asn Lys Gly Trp Leu Glu Leu Glu Ser Asp Pro Gly Leu Phe Thr
1 5 10 15

Leu Leu Val Glu Asp Phe Gly Val Lys Gly Val Gln Val Glu Glu Ile
20 25 30

Tyr Asp Leu Gln Ser Lys Cys Gln Gly Pro Val Tyr Gly Phe Ile Phe 35 40 45

Leu Phe Lys Trp Ile Glu Glu Arg Arg Ser Arg Arg Lys Val Ser Thr 50 55 60

Leu Val Asp Asp Thr Ser Val Ile Asp Asp Asp Ile Val Asn Asn Met 65 70 75 80

Phe Phe Ala His Gln Leu Ile Pro Asn Ser Cys Ala Thr His Ala Leu 85 90 95

Leu Ser Val Leu Leu Asn Cys Ser Ser Val Asp Leu Gly Pro Thr Leu 100 105 110

Ser Arg Met Lys Asp Phe Thr Lys Gly Phe Ser Pro Glu Ser Lys Gly
115 120 125

Tyr Ala Ile Gly Asn Ala Pro Glu Leu Ala Lys Ala His Asn Ser His 130 135 140

Ala Arg Pro Glu Pro Arg His Leu Pro Glu Lys Gln Asn Gly Leu Ser

Ala Val Arg Thr Met Glu Ala Phe His Phe Val Ser Tyr Val Pro Ile 165 170 175





Thr Gly Arg Leu Phe Glu Leu Asp Gly Leu Lys Val Tyr Pro Ile Asp 180 185 190

His Gly Pro Trp Gly Glu Asp Glu Glu Trp Thr Asp Lys Ala Arg Arg 195 200 205

Val Ile Met Glu Arg Ile Gly Leu Ala Thr Ala Gly Glu Pro Tyr His 210 215 220

Asp Ile Arg Phe Asn Leu Met 225 230

<210> 59

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:poly Gly flexible linker

<220>

<221> MOD_RES

<222> (6)..(200)

<223> Gly residues from position 6 to 200 may be present or absent

<400> 59





Gly Gly Gly Gly Gly Gly Gly 195 200

<210> 60

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DEAD box conserved motif

<400> 60 Asp Glu Ala Asp